



SEQUENCE LISTING

<110> ISAKO, HIROYUKI
MATSUMURA, KENJI
SHIMIZU, MASATOSHI
ITO, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTANOATE

<130> 72249

<140> US 10/004,115

<141> 2001-12-06

<150> JP 2000-372704

<151> 2000-12-07

<150> JP 2001-006144

<151> 2001-01-15

<150> JP 2001-026594

<151> 2001-02-02

<150> JP 2001-175175

<151> 2001-06-11

<160> 33

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 325

<213> PENICILLIUM CITRINUM

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			20					25					30		
Tyr	Thr	Ala	Val	Thr	Thr	Ala	Leu	Lys	Thr	Gly	Tyr	Arg	His	Leu	Asp
		35					40					45			
Cys	Ala	Trp	Tyr	Tyr	Leu	Asn	Glu	Gly	Glu	Val	Gly	Glu	Gly	Ile	Arg
	50					55					60				
Asp	Phe	Leu	Lys	Glu	Asn	Pro	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Val
65					70				75					80	
Cys	Thr	Lys	Val	Trp	Asn	His	Leu	His	Arg	Tyr	Glu	Asp	Val	Leu	Trp
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Ser	Ile	Asp	Asp	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Met
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Phe	Leu	Val	His	Trp	Pro	Ile	Ala	Ala	Glu	Lys	Asn	Gly	Gln	Gly	Glu
		115					120					125			
Pro	Lys	Ile	Gly	Pro	Asp	Gly	Lys	Tyr	Val	Ile	Leu	Lys	Asp	Leu	Thr
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Glu	Asn	Pro	Glu	Pro	Thr	Trp	Arg	Ala	Met	Glu	Lys	Ile	Tyr	Glu	Asp
145					150					155				160	
Arg	Lys	Ala	Arg	Ser	Ile	Gly	Val	Ser	Asn	Trp	Thr	Ile	Ala	Asp	Leu
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Glu	Lys	Met	Ser	Lys	Phe	Ala	Lys	Val	Met	Pro	His	Ala	Asn	Gln	Ile
			180					185						190	

Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
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 Lys Asn Leu Ser Ala
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 <212> DNA
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<220>
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 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30
 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45
 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 50 55 60
 gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80
 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95
 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110
 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag 384
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125
 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr

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Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp			
145	150	155	160
cgc aag gcc agg tcc att ggt gtc tca aac tgg acc att gcc gac ctt			528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu			
	165	170	175
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc			576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile			
	180	185	190
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc			624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe			
	195	200	205
tcc aag aac att atg ccc gtg gcc tac tct cct ctg gcc tgc cag aac			672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn			
	210	215	220
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Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn			
	225	230	235
gag atc gcc gag aag gcc gcc aac acc ctt gct cag gtt ctt att gcc			768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala			
	245	250	255
tgg ggt ctg cgc cgt gcc tac gtc gtt ctc ccc aag agc tcc aac ccc			816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro			
	260	265	270
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac			864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp			
	275	280	285
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc			912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val			
	290	295	300
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc			960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala			
	305	310	315
aag aac ctg tct gcg tga			978
Lys Asn Leu Ser Ala *			
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<210> 3
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 <212> PRT
 <213> PENICILLIUM CITRINUM

<400> 3
 Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val
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<210> 4

<211> 10
 <212> PRT
 <213> PENICILLIUM CITRINUM

 <400> 4
 Ile Phe Gly Val Phe Gly Thr Phe Ala Ser
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<210> 5

 <400> 5
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<210> 6
 <211> 14
 <212> PRT
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 <400> 6
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<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED
 OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 8
 ggaacytgrrt tytggsuacc 20

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 9
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<210> 10
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 <213> Artificial Sequence

<220>
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<210> 11
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<400> 13
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<400> 14
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<210> 15
<211> 697
<212> DNA
<213> ESCHERICHIA COLI

<400> 15
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aanactttca cactgagcaa cggcggtcaaa attcctggcg tcggttttgg tacctncgct      120
agtgaaggtt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccgggttac      180
cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnctcgt      240
gacttcctga aggaaaaccc ctcggtgaag cgtgaggaca tcttcgtctg caccaaggtg      300
tggaaccacc tccaccgtta tgaggacgtc ctctgggtcca ttgacnactc cctgaagcgt      360
cttggacttg actacgttga tatgttctct gttcactggc ccattgetgc cgaaaaaaat      420
ggccagggtg agcccaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc      480
gaaanccena ncccacctgg cgcgctatgg aaaaaatttn tngatccc aaggccaggt      540
ccattggtgt ttccaattgg accattgccc accttgagaa gatgtccaag ttngccaagg      600
tnatgctca cgccaaccag atcgagattc accccttctt gcccaacgag gagctggtgc      660
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<210> 16

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<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 16
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<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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 OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 17
 caaccagatc gagattcacc 20

<210> 18
 <211> 331
 <212> DNA
 <213> ESCHERICHIA COLI

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 ggctttggta ccttcgctag tgaaggttcc aagggcgaga cctatactgc tgtcaccact 180
 gccctgaaga ccggttaccc tcaattggac tgtgcctggc actacctgaa cgagggtgag 240
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<210> 19
 <211> 743
 <212> DNA
 <213> ESCHERICHIA COLI

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 cgggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac 180
 ccttgctcag gttcttattg cctggggctc gcgccgtggc tacgtcgttc tccccaagag 240
 ctccaacccc aagcgcattg agtccaactt caagagcatt gagctctccg atgccgactt 300
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 gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatnccc aaaanttttg 480
 agggtttctt gggtgaaaac gtttantgan cccgaantga angaatagat gancntgatt 540
 tctccaaaaa aaaaaaaaaa aaaaacggtc cgcggccgct ccnngggggg gcccggttcc 600
 caattcnccc cttatnattg aattcttttt taanggggnc aaattccncc nnatttcctt 660
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 <213> Artificial Sequence

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED
OLIGONUCLEOTIDE PRIMER FOR PCR

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<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED
OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 21
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<210> 22
<211> 417
<212> DNA
<213> ESCHERICHIA COLI

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agaagaatgg ccagggtgag cccaagattg gccctgacgg caaatacgtc attctcaagg 180
acctgaccga gaaccccgag ccacatggc gcgctatgga gaagatttat gaggatcgca 240
aggccaggtc cattggtgtc tccaactgga ccattgccja ccttgagaag atgtccaagt 300
tcgccaaggt catgcctcac gccaacaga tcgagattca ccccttcctg cccaacgagg 360
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<210> 23
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 23
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<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED
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<400> 24
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<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> DESCRIPTION OFARTIFICIAL SEQUENCE: DESIGNED

OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 25
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<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<210> 27
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<212> DNA
<213> ESCHERICHIA COLI

<220>
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acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
20 25 30
aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt 144
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
35 40 45
tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
50 55 60
gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att 240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
65 70 75 80
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
85 90 95
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
100 105 110
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att 384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115 120 125
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg 432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
130 135 140

agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
148 150 155 160	

agt aaa ggt gga atg aag ctg atg acg gaa aca cct gca tta gaa tat	518
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	

gct cca aaa ggt att cgt gta aat aac att gga cag gga gag att aat	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	

aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	

gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	

gca gag gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	

ggg att aca ctg ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	

caa gca gga ccg gga taa	786
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<210> 28
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<220>
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 <222> (1)... (978)

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Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp 35 90 95	238
tcc att gag gac tcc cgt aag cgt ctt gga ctt gag tac gln gat atg Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met 100 105 110	336
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ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr 130 135 140	432
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp 145 150 155 160	430
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu 165 170 175	523
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile 180 185 190	576
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe 195 200 205	624
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tgc cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn 210 215 220	672
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn 225 230 235 240	720
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala 245 250 255	768
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro 260 265 270	816
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp 275 280 285	864
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<210> 29
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<220>
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<210> 30
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<220>
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 OLIGONUCLEOTIDE PRIMER FOR PCR

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<210> 32
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<220>
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<400> 32
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<210> 33
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 <212> DNA
 <213> Artificial Sequence

<220>
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28

<210> 34
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 <212> PRT
 <213> CORYNEBACTERIUM SP.

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 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 20 25 30
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 35 40 45
 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly

50	Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile
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80	His	Cys	Ser	Gln	Gly	Leu	Gln	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu
95	Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe
110	Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp
125	Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His
140	Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val
155	Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg
170	His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys
185	Leu	Glu	Leu	Ala	Thr	Lys	Val	Gly	Ala	His	Glu	Val	Val	Leu	Ser	Asp
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215	Ala	Leu	Val	Leu	Asp	Phe	Val	Gly	Tyr	Gln	Pro	Thr	Ile	Asp	Thr	Ala
230	Met	Ala	Val	Ala	Gly	Val	Gly	Ser	Asp	Val	Thr	Ile	Val	Gly	Ile	Gly
245	Asp	Gly	Gln	Ala	His	Ala	Lys	Val	Gly	Phe	Phe	Gln	Ser	Pro	Tyr	Glu
260	Ala	Ser	Val	Thr	Val	Pro	Tyr	Trp	Gly	Ala	Arg	Asn	Glu	Leu	Ile	Glu
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290	Leu	Gln	Ser	Arg	Gln	Arg	Cys	Arg	Ser	Val	Ser	Thr	Thr	Gly	Cys	Arg
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320	Ala	Val	Glu	Arg	Gln	Arg	Lys	Asn	Thr	Asp	Ala	Arg	Pro	Asn	Ser	Ile
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gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc	96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val	
20 25 30	
acc gct gct ggc gtc tgc cac tgc gac gac ttc atc atg agc ctg ccc	144

Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro		
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gaa	gag	cag	tac	acc	tac	ggc	ctt	ccg	ctc	acc	ctc	ggc	cac	gaa	ggc		192
Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly		
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Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile		
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gga	acc	aat	gtc	gtc	gtc	tac	ggg	cct	tgg	ggg	tgc	ggc	aac	tgt	tgg		288
Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Asn	Cys	Trp		
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cac	tgc	tca	caa	gga	ctc	gag	aac	tat	tgc	tct	cgc	gcc	caa	gaa	ctc		336
His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu		
			100					105						110			
gga	atc	aat	cct	ccc	ggg	ctc	ggg	gca	ccc	ggc	gag	ttg	gcc	gag	ttc		384
Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe		
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atg	atc	gtc	gat	tct	cct	cgc	cac	ctt	gtc	ccg	atc	ggg	gac	ctc	gac		432
Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp		
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ccg	gtc	aag	acg	gtg	ccg	ctg	acc	gac	gcc	ggg	ctg	acg	ccg	tat	cac		480
Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His		
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Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val		
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gtc	att	ggg	acc	ggc	ggg	ctc	ggc	cac	gtc	gct	att	cag	ctc	ctc	cgc		576
Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg		
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cac	ctc	tgc	gcg	gca	acg	gtc	atc	gct	ttg	gac	gtg	agc	gcg	gac	aag		624
His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys		
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ctc	gaa	ctg	gca	acc	aag	gta	ggc	gct	cac	gaa	gtg	gtt	ctg	tcc	gac		672
Leu	Glu	Leu	Ala	Thr	Lys	Val	Gly	Ala	His	Glu	Val	Val	Leu	Ser	Asp		
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aag	gac	gcg	gcc	gag	aac	gtc	cgc	aag	atc	act	gga	agt	caa	ggc	gcc		720
Lys	Asp	Ala	Ala	Glu	Asn	Val	Arg	Lys	Ile	Thr	Gly	Ser	Gln	Gly	Ala		
	225				230				235					240			
gca	ttg	gtt	ctc	gac	ttc	gtc	ggc	tac	cag	ccc	acc	atc	gac	acc	gcg		768
Ala	Leu	Val	Leu	Asp	Phe	Val	Gly	Tyr	Gln	Pro	Thr	Ile	Asp	Thr	Ala		
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atg	gct	gtc	gcc	ggc	gtc	gga	tca	gac	gtc	acg	atc	gtc	ggg	atc	ggg		816
Met	Ala	Val	Ala	Gly	Val	Gly	Ser	Asp	Val	Thr	Ile	Val	Gly	Ile	Gly		
			260					265					270				
gac	ggc	cag	gcc	cac	gcc	aaa	gtc	ggg	ttc	ttc	caa	agt	cct	tac	gag		864
Asp	Gly	Gln	Ala	His	Ala	Lys	Val	Gly	Phe	Phe	Gln	Ser	Pro	Tyr	Glu		
		275					280					285					

gct	tty	gtg	aca	gtt	ccg	tat	tgg	gat	gac	ccc	aac	gag	ccg	atc	gaa	910
Ala	Ser	Val	Thr	Val	Pro	Tyr	Trp	Gly	Ala	Arg	Asn	Gln	Ile	Ile	Gln	
290					295					300						
ttg	atc	gac	ctc	gcc	cac	gat	ggc	atc	tcc	gac	atc	ggt	gat	caa	gac	960
Ile	Ile	Arg	Ile	Ala	His	Ala	Gly	Ile	Phe	Asp	Ile	Gly	Gly	Gly	Arg	
305				310					315						320	
ctt	cag	tct	cga	caa	egg	tgc	cga	agg	gta	tcc	acc	act	ggc	tgt	egg	1008
Leu	Gln	Ser	Arg	Gln	Arg	Cys	Arg	Ser	Val	Ser	Thr	Thr	Gly	Cys	Arg	
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aac	gct	cag	egg	ccg	tgc	ggt	tgt	ggt	ccc	tgg	tct	gta	gta	ccg	aca	1036
Asn	Ala	Gln	Arg	Pro	Cys	Gly	Cys	Gly	Pro	Trp	Ser	Val	Val	Pro	Thr	
			340					345					350			
ggc	gta	gaa	cga	cag	egg	aaa	aac	act	gat	gcc	egg	ccg	aat	tcc	att	1104
Ala	Val	Glu	Arg	Gln	Arg	Lys	Asn	Thr	Asp	Ala	Arg	Pro	Asn	Ser	Ile	
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egg	ccg	ggc	atc	agt	gtc	aga	aat	tcc	gtg	tgc	gct	agc	tgc	acg	cct	1152
Arg	Pro	Gly	Ile	Ser	Val	Arg	Asn	Ser	Val	Cys	Ala	Ser	Cys	Thr	Pro	
	370					375					380					
cga	tga															1158
Arg	*															
385																